

WHAT IS CLAIMED IS:

1. A method for genotyping comprising the steps of:

(a) obtaining nucleic acid material from a genome;

(b) amplifying locations of the material;

(c) assaying the amplified material based on size and concentration;

(d) converting the assayed amplified material into a first set of electrical signals corresponding to size and concentration of the amplified material at the locations; and

(e) operating on the first set of electrical signals produced from the amplified material with a second set of electrical signals corresponding to response patterns of the locations to produce a third set of clean electrical signals corresponding to the size and multiplicities of the unamplified material on the genome at the locations.

2. A method as described in Claim 1 wherein the second set of electrical signals corresponds to a PCR stutter response pattern of the location.

3. A method as described in Claim 1 wherein the operating step on the first set of electrical signals with the second set of electrical signals includes the step of a deconvoluting the first set of electrical signals with the second set of electrical signals.

4. A method as described in Claim 1 wherein the operating step on the first set of electrical signals with the second set of electrical signals includes the step of deconvolving using computed properties of the electrical signals.

5. A method as described in Claim 1 wherein the operating step on the first set of electrical signals with the second set of electrical signals includes the step of deconvolving with matrix processing using computed properties of the electrical signals.

6. A method as described in Claim 1 wherein the determination of the second set of electrical signals of the location comprising the steps of:

- (a) obtaining nucleic acid material from a genome;
- (b) amplifying locations of the material;
- (c) assaying the amplified material based on size and concentration;
- (d) converting the assayed amplified material into a first set of electrical signals corresponding to size and concentration of the amplified material at the locations; and
- (e) operating on the first set of electrical signals produced from the amplified material to produce a second set of electrical signals corresponding to response patterns of the locations.

7. A method as described in Claim 1 wherein the obtaining step pools nucleic acid material from one or more individuals.

8. A method as described in Claim 1 wherein the amplifying step uses more than one location.

9. A method as described in Claim 1 wherein the amplifying step uses more than one location, and the size properties of these locations are not necessarily disjoint.

10. A method as described in Claim 1 wherein the amplifying step uses more than one location, the size properties of these locations are not necessarily disjoint, and the first set of electrical signals shows concentrations of the amplified material from different locations having the same size.

11. A method as described in Claim 1 wherein the amplifying step uses more than one location, the size properties of these locations are not necessarily disjoint, the first set of electrical signals shows concentrations of the amplified material from different locations having the same size, and the PCR stutter patterns of the different locations provide the primary mechanism for genotyping the locations.

12. A method as described in Claim 1 wherein the operating step makes use of a second set of electrical signals corresponding to response patterns of the locations.

13. A system for genotyping comprising:

(a) means or mechanism for obtaining nucleic acid material from a genome;

(b) means or mechanism for amplifying locations of the material, said amplifying means or mechanism in communication with the nucleic acid material;

(c) means or mechanism for assaying the amplified material based on size and concentration, said assaying means or mechanism in communication with amplifying means or mechanism;

(d) means or mechanism for converting the assayed amplified material into a first set of electrical signals corresponding to size and concentration of the amplified material at the locations, said converting means or mechanism in communication with the assaying means; and

(e) means or mechanism for operating on the first set of electrical signals produced from the amplified material with a second set of electrical signals corresponding to a response pattern of the locations to produce a third set of clean electrical signals corresponding to the size and multiplicities of the unamplified material on the genome at the locations, said operating means or mechanism in communication with the sets of electrical signals.

14. A system as described in Claim 13 wherein:

(a) the amplifying means or mechanism includes polymerase chain reaction, or harvesting cloned cells;

(b) the assaying means or mechanism includes gel or ultrathin gel electrophoresis, or mass spectroscopy, or denaturing gradient gel electrophoresis, or differential hybridization, or sequencing by hybridization;

(c) the converting means or mechanism employs labeling with detection including radioactivity, or fluorescence, or phosphorescence, or chemiluminescence, or visible light, or ions, or pH, or electricity, or resistivity, or biotinylation, or antibodies; and includes the detecting means or mechanism which includes a photomultiplier tube; a radioactivity counter, a resistivity sensor, a pH meter, or an optical detector; and

(d) the operating means or mechanism includes statistical moment determinations, or Fourier transformation, or optimal filtering, or polynomial calculations, or matrix computations.

15. A method for analyzing genetic material of an organism comprising the steps of:

(a) amplifying the genetic material;

(b) assaying size and concentration features of the amplified genetic material; and

(c) characterizing the amplified genetic material in a region having a radius of less than five feet at a rate exceeding 100 polynucleotide genetic markers per hour.

